

SEQUENCE LISTING

<110> Chandrashekar, Ramaswamy
Morales, Tony H.

<120> Parasitic Helminth Cuticlin Proteins, Nucleic Acid
Molecules, and Uses Thereof

<130> HW-8

<140> not yet assigned

<141> 1999-06-01

<150> 60/087,435

<151> 1998-06-01

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<170> PatentIn Ver. 2.0

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Cys Gly Pro Thr Ser Ile Thr Ile Asn Phe Asn Thr Arg Asn Ala Phe
35 40 45
gaa gga cat gtt tat gtg aaa ggt ctt tat gat caa gaa ggt tgc cgt 192
Glu Gly His Val Tyr Val Lys Gly Leu Tyr Asp Gln Glu Gly Cys Arg
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aat gat gaa ggt gga cgt caa gtt gcc gga att tca ott cca ttt gat 240
Asn Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp
65 70 75 80
tca tgc aat gtt gcg cgt aca cga tct ctg aat cca cgt ggt att ttt 288
Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe
85 90 95
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Val Thr Thr Thr Val Val Ile Ser Phe His Pro Leu Phe Val Thr Lys
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225 230 235 240	
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Thr Ile Lys Glu Pro Asn Ser Glu Cys Val Arg Pro Gln Cys Ser Glu	
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Pro Gln Gly Phe Gly Ala Val Lys Thr Gly Gly Ala Ala Ala Lys Pro	
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Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala
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Val Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Thr Val Glu
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Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile	145	150	155	160
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Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala	165	170	175	
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<213> *Dirofilaria immitis*

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Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu
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Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala Asp Arg Ser Glu
 115 120 125

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Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala
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Pro Glu Ala Ser Leu Leu Ser Pro Arg Leu Ile Lys Lys Arg Ser Ile
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Asn Ser Asp Asn Thr Val Asp Val Ser Thr Gly Phe Ser Thr Val Asp
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Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser
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Thr Ser Arg Glu Gln Phe Asn Gly Ile Phe Cys Ile Ala Ser Asn Asp
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<213> *Dirofilaria immitis*

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 taacatagca ccgaacaaaa tgataagtaa aatatcattt gatgcaatac agaagatacc 120
 attgaattgt tcacggctcg ttgatgatga taaacgattt gctgagaagt tcggattctc 180
 ttcggttata tcaaccgtgc taaaaccggt actgaogtcc accgtattat cagaattaat 240
 tgatcgcttc ttgatcaatc gtggagaaaag caaggaagct tctggagctg gtgcagcagc 300
 agattttaca gcagcaaatc cttgtccaga ttttatggca ccaaatacctt gtggctctgt 360
 gcattgtggt cgaggacatt cgctatgtgg ctctttaatt gttatactaa tctggcattg 420
 atagtaaagt tctgatcgat ctgcatattt ataaacatga gcttottggc cagccattaa 480
 atctgtaata tattccaaat tattgagtaa atattgtcc aaagcacatc cttcttcatt 540
 cagaatctcc actgcatcac cttttccatc atccacaaca catgaatgta ctaatgcaca 600
 gaatgtatct gtagtctctg aatcacatgt ccatttgtga tatacatgat ctccaatcat 660
 tgcaaatcga acaggtgcac cagttggtcc accttccaaa atctcatatc gacatacggg 720
 cattggtacc acttgagttt ggaatgctgt agtcatttca gatacttcaa ggaccagtac 780
 taacggtctt atcagctttc catataaaaa cat 813

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11
ggctggccaa gaagctcacg tatacaaata tgcg 34

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12
cgcatatttg tatacgtgag cttcttggcc agcc 34

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13
ggtttaatta cccaagtttg ag 22

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14
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<210> 15
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 15
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<210> 16
<211> 892
<212> DNA
<213> Brugia malayi

<220>
<221> CDS
<222> (158)..(892)

<400> 16
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gcaatttcaa attaatacatt ttgctaattc tattattcca actattttca tcaataatca 120
ctgagaagaa atcaggaaga aagaagcaaa aagtttaa atg ttg cat atg caa att 175
Met Leu His Met Gln Ile
1 5

tgc tca ttt ttg tca tat atg ata ata gca agt att aat gct att cca 223
Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala Ser Ile Asn Ala Ile Pro
10 15 20

att gat aat ggt gtc gaa agt gaa cct gaa att gaa tgt ggt cca aca 271
Ile Asp Asn Gly Val Glu Ser Glu Pro Glu Ile Glu Cys Gly Pro Thr
25 30 35

tca atc act gtt aat ttt aat act cga aat cct ttt gaa gga cat gta 319
Ser Ile Thr Val Asn Phe Asn Thr Arg Asn Pro Phe Glu Gly His Val
40 45 50

tat gct aaa gga tta tac agt aat caa gat tgt cgt agt gat gaa ggt 367

Tyr	Ala	Lys	Gly	Leu	Tyr	Ser	Asn	Gln	Asp	Cys	Arg	Ser	Asp	Glu	Gly		
55					60					65					70		
gga	cgt	cag	gta	gcc	gga	ata	tca	tta	ccg	ttt	gat	tca	tgt	aat	gtc	415	
Gly	Arg	Gln	Val	Ala	Gly	Ile	Ser	Leu	Pro	Phe	Asp	Ser	Cys	Asn	Val		
				75					80					85			
gca	cgt	aca	cgt	tcg	tta	aat	cca	cgt	gga	ata	ttt	gtc	aca	gct	gtt	463	
Ala	Arg	Thr	Arg	Ser	Leu	Asn	Pro	Arg	Gly	Ile	Phe	Val	Thr	Ala	Val		
				90					95				100				
gtg	gta	att	acg	ttt	cat	cca	cag	ttt	atc	aca	aaa	gtt	gat	cga	aca	511	
Val	Val	Ile	Thr	Phe	His	Pro	Gln	Phe	Ile	Thr	Lys	Val	Asp	Arg	Thr		
		105						110					115				
tat	cga	ttg	caa	tgc	ttt	tac	atg	gaa	gct	gat	aag	act	gtt	agc	aca	559	
Tyr	Arg	Leu	Gln	Cys	Phe	Tyr	Met	Glu	Ala	Asp	Lys	Thr	Val	Ser	Thr		
		120					125					130					
caa	att	gaa	gtt	tcc	gaa	atg	aca	acc	gta	ttt	gct	aca	caa	ttg	gta	607	
Gln	Ile	Glu	Val	Ser	Glu	Met	Thr	Thr	Val	Phe	Ala	Thr	Gln	Leu	Val		
		135				140					145				150		
cca	atg	cct	gtg	tgt	aga	tat	gag	att	ctg	gat	ggg	ggg	cca	acc	gga	655	
Pro	Met	Pro	Val	Cys	Arg	Tyr	Glu	Ile	Leu	Asp	Gly	Gly	Pro	Thr	Gly		
				155					160					165			
caa	cct	gtc	cag	tat	gct	aat	att	gga	caa	ccg	gtt	tat	cat	aaa	tgg	703	
Gln	Pro	Val	Gln	Tyr	Ala	Asn	Ile	Gly	Gln	Pro	Val	Tyr	His	Lys	Trp		
			170					175					180				
aca	tgt	gat	tct	gaa	aca	gtt	gat	acc	ttc	tgt	gct	ttg	gta	cat	tcc	751	
Thr	Cys	Asp	Ser	Glu	Thr	Val	Asp	Thr	Phe	Cys	Ala	Leu	Val	His	Ser		
		185						190					195				
tgt	ttt	gtt	gat	gat	ggc	aat	ggg	gac	agt	att	aat	tta	att	aat	gaa	799	
Cys	Phe	Val	Asp	Asp	Gly	Asn	Gly	Asp	Ser	Ile	Asn	Leu	Ile	Asn	Glu		
		200					205					210					
gaa	gga	tgt	gca	tta	gat	cga	tat	ott	cta	aat	aat	ttg	gaa	tat	cca	847	
Glu	Gly	Cys	Ala	Leu	Asp	Arg	Tyr	Leu	Leu	Asn	Asn	Leu	Glu	Tyr	Pro		
		215				220					225				230		
act	gat	cta	atg	gct	ggc	caa	gaa	gct	cac	gta	tac	aaa	tat	gcg		892	
Thr	Asp	Leu	Met	Ala	Gly	Gln	Glu	Ala	His	Val	Tyr	Lys	Tyr	Ala			
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<210> 17

<211> 245

<212> PRT

<213> Brugia malayi

<400> 17

Met Leu His Met Gln Ile Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala
1 5 10 15

Ser Ile Asn Ala Ile Pro Ile Asp Asn Gly Val Glu Ser Glu Pro Glu
20 25 30

Ile Glu Cys Gly Pro Thr Ser Ile Thr Val Asn Phe Asn Thr Arg Asn
35 40 45

Pro Phe Glu Gly His Val Tyr Ala Lys Gly Leu Tyr Ser Asn Gln Asp
50 55 60

Cys Arg Ser Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro
65 70 75 80

Phe Asp Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly
85 90 95

Ile Phe Val Thr Ala Val Val Val Ile Thr Phe His Pro Gln Phe Ile
100 105 110

Thr Lys Val Asp Arg Thr Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala
115 120 125

Asp Lys Thr Val Ser Thr Gln Ile Glu Val Ser Glu Met Thr Thr Val
130 135 140

Phe Ala Thr Gln Leu Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu
145 150 155 160

Asp Gly Gly Pro Thr Gly Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln
165 170 175

Pro Val Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe
180 185 190

Cys Ala Leu Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Ser
195 200 205

Ile Asn Leu Ile Asn Glu Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu
210 215 220

Asn Asn Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His
 225 230 235 240

Val Tyr Lys Tyr Ala
 245

<210> 18
 <211> 892
 <212> DNA
 <213> Brugia malayi

<400> 18
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 attgccatca tcaacaaaac aggaatgtac caaagcacag aaggtatcaa ctgtttcaga 180
 atcacatgtc catttatgat aaaccgggtg tccaatatta gcatactgga caggttgtcc 240
 ggttggacca ccatccagaa tctcatatct acacacaggc attggtacca attgtgtagc 300
 aaatacgggtt gtcatttcgg aaacttcaat ttgtgtgcta acagtcttat cagcttccat 360
 gtaaaagcat tgcaatcgat atgttcgatc aacttttgtg ataaactgtg gatgaaacgt 420
 aattaccaca acagctgtga caaatattcc acgtggattt aacgaacgtg tacgtgcgac 480
 attacatgaa tcaaacggta atgatattcc ggctacctga cgtccacctt catcactacg 540
 acaatcttga ttactgtata atcctttagc atatacatgt ccttcaaaag gatttcgagt 600
 attaaaatta acagtgattg atgttggacc acattcaatt tcaggttcac tttcgacacc 660
 attatcaatt ggaatagcat taatacttgc tattatcata tatgacaaaa atgagcaaatt 720
 ttgcatatgc aacatttaac tttttgcttc tttcttcctg atttcttctc agtgattagt 780
 gatgaaaata gttggaataa tagaattagc aaaatgatta atttgaaatt gcaacaaatt 840
 attgaattat tgatgatcaa ttttaatgat ctcaaacttg ggtaattaa cc 892